

**We claim:**

1. A substantially purified nucleic acid molecule that encodes a maize or soybean carbon assimilation pathway enzyme or fragment thereof, wherein said maize or soybean carbon assimilation pathway enzyme is selected from the group consisting of:

- (a) ribulose-bisphosphate carboxylase;
- (b) phosphoglycerate kinase;
- (c) glyceraldehyde 3-phosphate dehydrogenase;
- (d) putative glyceraldehyde 3-phosphate dehydrogenase;
- (e) triose phosphate isomerase;
- (f) aldolase;
- (g) fructose-1,6-bisphosphatase;
- (h) transketolase;
- (i) putative transketolase;
- (j) sedoheptulose-1,7-bisphosphatase;
- (k) D-ribulose-5-phosphate-3-epimerase;
- (l) ribose-5-phosphate isomerase;
- (m) putative ribose-5-phosphate isomerase;
- (n) ribose-5-phosphate kinase;
- (o) phosphoenolpyruvate carboxylase;
- (p) NADP-dependent malate dehydrogenase;
- (q) aspartate aminotransferase;
- (r) putative aspartate aminotransferase;
- (s) alanine aminotransferase;
- (t) NADP-dependent malic enzyme;
- (u) NAD-dependent malic enzyme;
- (v) PEP carboxykinase;

- (w) putative PEP carboxykinase;
- (x) pyruvate, phosphate dikinase; and
- (y) pyrophosphatase.

2. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 7341.

3. A substantially purified maize or soybean carbon assimilation pathway enzyme or fragment thereof, wherein said maize or soybean carbon assimilation pathway enzyme is selected from the group consisting of

- (a) ribulose-bisphosphate carboxylase or fragment thereof;
- (b) phosphoglycerate kinase or fragment thereof;
- (c) glyceraldehyde 3-phosphate dehydrogenase or fragment thereof;
- (d) putative glyceraldehyde 3-phosphate dehydrogenase or fragment thereof;
- (e) triose phosphate isomerase or fragment thereof;
- (f) aldolase or fragment thereof;
- (g) fructose-1,6-bisphosphatase or fragment thereof;
- (h) transketolase or fragment thereof;
- (i) putative transketolase or fragment thereof;
- (j) sedoheptulose-1,7-bisphosphatase or fragment thereof;
- (k) D-ribulose-5-phosphate-3-epimerase or fragment thereof;

- (l) ribose-5-phosphate isomerase or fragment thereof;
- (m) putative ribose-5-phosphate isomerase or fragment thereof;
- (n) ribose-5-phosphate kinase or fragment thereof;
- (o) phosphoenolpyruvate carboxylase or fragment thereof;
- (p) NADP-dependent malate dehydrogenase or fragment thereof;
- (q) aspartate aminotransferase or fragment thereof;
- (r) putative aspartate aminotransferase or fragment thereof;
- (s) alanine aminotransferase or fragment thereof;
- (t) NADP-dependent malic enzyme or fragment thereof;
- (u) NAD-dependent malic enzyme or fragment thereof;
- (v) PEP carboxykinase or fragment thereof;
- (w) putative PEP carboxykinase;
- (x) pyruvate, phosphate dikinase or fragment thereof; and
- (y) pyrophosphatase or fragment thereof.

4. A substantially purified maize or soybean carbon assimilation pathway enzyme or fragment thereof according to claim 3, wherein said maize or soybean carbon assimilation pathway enzyme or fragment thereof is encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 7341.

5. A substantially purified antibody or fragment thereof which is capable of specifically binding to a specific maize or soybean carbon assimilation pathway enzyme or fragment thereof according to claim 4.

6. A transformed plant having a nucleic acid molecule which comprises:

(A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule;

(B) a structural nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

(a) a nucleic acid sequence which encodes for a ribulose-bisphosphate carboxylase enzyme or fragment thereof;

(b) a nucleic acid sequence which encodes for a phosphoglycerate kinase enzyme or fragment thereof;

(c) a nucleic acid sequence which encodes for a glyceraldehyde 3-phosphate dehydrogenase enzyme or fragment thereof;

(d) a nucleic acid sequence which encodes for a putative glyceraldehyde 3-phosphate dehydrogenase enzyme or fragment thereof;

(e) a nucleic acid sequence which encodes for a triose phosphate isomerase enzyme or fragment thereof;

(f) a nucleic acid sequence which encodes for a aldolase enzyme or fragment thereof;

(g) a nucleic acid sequence which encodes for a fructose-1,6-bisphosphatase enzyme or fragment thereof;

- (h) a nucleic acid sequence which encodes for a transketolase enzyme or fragment thereof;
- (i) a nucleic acid sequence which encodes for a putative transketolase enzyme or fragment thereof;
- (j) a nucleic acid sequence which encodes for a sedoheptulose-1,7-bisphosphatase enzyme or fragment thereof;
- (k) a nucleic acid sequence which encodes for a D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof;
- (l) a nucleic acid sequence which encodes for a ribose-5-phosphate isomerase enzyme or fragment thereof;
- (m) a nucleic acid sequence which encodes for a putative ribose-5-phosphate isomerase enzyme or fragment thereof;
- (n) a nucleic acid sequence which encodes for a ribose-5-phosphate kinase enzyme or fragment thereof;
- (o) a nucleic acid sequence which encodes for a phosphoenolpyruvate carboxylase enzyme or fragment thereof;
- (p) a nucleic acid sequence which encodes for a NADP-dependent malate dehydrogenase enzyme or fragment thereof;
- (q) a nucleic acid sequence which encodes for an aspartate aminotransferase enzyme or fragment thereof;
- (r) a nucleic acid sequence which encodes for a putative aspartate aminotransferase enzyme or fragment thereof;

- (s) a nucleic acid sequence which encodes for an alanine aminotransferase enzyme or fragment thereof;
- (t) a nucleic acid sequence which encodes for a NADP-dependent malic enzyme or fragment thereof;
- (u) a nucleic acid sequence which encodes for a NAD-dependent malic enzyme or fragment thereof;
- (v) a nucleic acid sequence which encodes for a PEP carboxykinase enzyme or fragment thereof;
- (w) a nucleic acid sequence which encodes for a putative PEP carboxykinase enzyme or fragment thereof;
- (x) a nucleic acid sequence which encodes for a pyruvate, phosphate dikinase enzyme or fragment thereof;
- (y) a nucleic acid sequence which encodes for a pyrophosphatase enzyme or fragment thereof;
- (z) a nucleic acid sequence which is complementary to any of the nucleic acid sequences of (a) through (y); and

(C) a 3' non-translated sequence that functions in said plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

7. The transformed plant according to claim 6, wherein said structural gene is complementary to any of the nucleic acid sequences of (a) through (y).

8. A method for determining a level or pattern in a plant cell of an carbon assimilation pathway enzyme in a plant metabolic pathway comprising:

(A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, said marker nucleic acid molecule selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 1 through SEQ ID NO: 7341 or compliments thereof, with a complementary nucleic acid molecule obtained from said plant cell or plant tissue, wherein nucleic acid hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue permits the detection of an mRNA for said carbon assimilation pathway enzyme;

(B) permitting hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue; and

(C) detecting the level or pattern of said complementary nucleic acid, wherein the detection of said complementary nucleic acid is predictive of the level or pattern of said carbon assimilation pathway enzyme in said plant metabolic pathway.

9. The method of claim 8, wherein said level or pattern is detected by *in situ* hybridization.